

JAP20 Rec'd PCT/PTO 19 JUL 2006

SEQUENCE LISTING

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<110> OncoMab GmbH et al.

<120> Neoplasm-Specific Polypeptides and Their Uses

<130> 50308/009W03

<150> 10/764,730
<151> 2004-01-26

<160> 30

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2118

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<221> CDS

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gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag att tat 96
 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
 20 25 30

cct gga agt ggt aat act tac tac aat gag aag ttc aag ggc aag gcc 144
 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
 35 40 45

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 35 40 45
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
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 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
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 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 20 25 30

tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg atc tac aaa 144
 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 35 40 45

gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 192
 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 50 55 60

tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat 240
 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 65 70 75 80

ctg gga gtt tat tac tgc ttt caa ggt tca cat gtt ccg tac acg ttc 288
 Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe
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 35 40 45
 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
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<213> Homo sapiens

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gtg gcc aga gag gtt tgc aaa tct act ata aca gag att gaa gaa tgt 144
 Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Glu Glu Cys
 35 40 45

gct gat gaa ccg gtt gga aaa ggt tac atg gtt tcc tgc ttg gtg gat 192
 Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp
 50 55 60

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 His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys
 65 70 75 80

atg acg gcc atc att ttt agt gat tac cgt tta atc tgt ggc ttc atg 288
 Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met
 85 90 95

gat gac tgc aaa aat gac atc aac att ctg aaa tgt ggc agt att cgg 336
 Asp Asp Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg
 100 105 110

ctt gga aag gat gca cat tca caa ggt gag gtg gta tca tgc ttg	384
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115 120 125	
gag aaa ggc ctg gtg aaa gaa gca gaa gaa aga gaa ccc aag att caa	432
Glu Lys Gly Leu Val Lys Glu Ala Glu Arg Glu Pro Lys Ile Gln	
130 135 140	
gtt tct gaa ctc tgc aag aaa gcc att ctc cgg gtg gct gag ctg tca	480
Val Ser Glu Leu Cys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser	
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Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp	
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Asp Arg Glu Arg Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val	
180 185 190	
tat aag tgc ctc ttt aac cat aaa ttt gaa gaa tcc atg agt gaa aag	624
Tyr Lys Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys	
195 200 205	
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Cys Arg Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr	
210 215 220	
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Lys Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys	
225 230 235 240	
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Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu	
245 250 255	
tcc tac ttg tta atg tgc ctg gag tca gct gta cac aga ggg cga caa	816
Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln	
260 265 270	
gtc agc agt gag tgc cag ggg gag atg ctg gat tac cga cgc atg ttg	864
Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu	
275 280 285	
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Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly	
290 295 300	
gag att gaa cac cat tgt tcc gga tta cat cga aaa ggg cgg acc cta	960
Glu Ile Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu	
305 310 315 320	
cac tgt ctg atg aaa gta gtt cga ggg gag aag ggg aac ctt gga atg	1008
His Cys Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met	
325 330 335	

aac tgc cag cag gcg ctt caa aca ctg att cag gag act gac cct ggt	1056		
Asn Cys Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly			
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gca gat tac cgc att gat cga gct ttg aat gaa gct tgt gaa tct gta	1104		
Ala Asp Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val			
355	360	365	
atc cag aca gcc tgc aaa cat ata aga tct gga gac cca atg atc ttg	1152		
Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu			
370	375	380	
tcg tgc ctg atg gaa cat tta tac aca gag aag atg gta gaa gac tgt	1200		
Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys			
385	390	395	400
gaa cac cgt ctc tta gag ctg cag tat ttc atc tcc cgg gat tgg aag	1248		
Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys			
405	410	415	
ctg gac cct gtc ctg tac cgc aag tgc cag gga gac gct tct cgt ctt	1296		
Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu			
420	425	430	
tgc cac acc cac ggt tgg aat gag acc agc gaa ttt atg cct cag gga	1344		
Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly			
435	440	445	
gct gtg ttc tct tgt tta tac aga cac gcc tac cgc act gag gaa cag	1392		
Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln			
450	455	460	
gga agg agg ctc tca cgg gag tgc cga gct gaa gtc caa agg atc cta	1440		
Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu			
465	470	475	480
cac cag cgt gcc atg gat gtc aag ctg gat cct gcc ctc cag gat aag	1488		
His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys			
485	490	495	
tgc ctg att gat ctg gga aaa tgg tgc agt gag aaa aca gag act gga	1536		
Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly			
500	505	510	
cag aag ctg gag tgc ctt cag gac cat ctg gat gac tta gtg gtg gag	1584		
Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu			
515	520	525	
tgt aga gat ata gtt ggc aac ctc act gag tta gaa tca gag gat att	1632		
Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile			
530	535	540	
caa ata gaa gcc ttg ctg atg aga gcc tgt gag ccc ata att cag aac	1680		
Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn			
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ttc tgc cac gat gtg gca gat aac cag ata gac tcc ggg gac ctg atg	1728		

Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met	565	570	575	
gag tgt ctg ata cag aac aaa cac cag aag gac atg aac gag aag tgt				1776
Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys				
580	585	590		
gcc atc gga gtt acc cac ttc cag ctg gtg cag atg aag gat ttt cgg				1824
Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg				
595	600	605		
ttt tct tac aag ttt aaa atg gcc tgc aag gag gac gtg ttg aag ctt				1872
Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu				
610	615	620		
tgc cca aac ata aaa aag aag gtg gac gtg atc tgc ctg agc acg				1920
Cys Pro Asn Ile Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr				
625	630	635	640	
acc gtg cgc aat gac act ctg cag gaa gcc aag gag cac agg gtg tcc				1968
Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser				
645	650	655		
ctg aag tgc cgc agg cag ctc cgt gtg gag gag ctg gag atg acg gag				2016
Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu				
660	665	670		
gac atc cgc ttg gag cca gat cta tac gaa gcc tgc aag agt gac atc				2064
Asp Ile Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile				
675	680	685		
aaa aac ttc tgt tcc gct gtg caa tat ggc aac gct cag att atc gaa				2112
Lys Asn Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu				
690	695	700		
tgt ctg aaa gaa aac aag cag cta agc acc cgc tgc cac caa aaa				2160
Cys Leu Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys				
705	710	715	720	
gta ttt aag ctg cag gag aca gag atg atg gac cca gag cta gac tac				2208
Val Phe Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr				
725	730	735		
acc ctc atg agg gtc tgc aag cag atg ata aag aag ttc tgt ccg gaa				2256
Thr Leu Met Arg Val Cys Lys Gln Met Ile Lys Lys Phe Cys Pro Glu				
740	745	750		
gca gat tct aaa acc atg ttg cag tgc ttg aag caa aat aaa aac agt				2304
Ala Asp Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser				
755	760	765		
gaa ttg atg gat ccc aaa tgc aaa cag atg ata acc aag cgc cag atc				2352
Glu Leu Met Asp Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile				
770	775	780		
acc cag aac aca gat tac cgc tta aac ccc atg tta aga aaa gcc tgt				2400
Thr Gln Asn Thr Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys				

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785	790	795	800	
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gat gat tca gaa tta gaa gga caa gtc atc tct tgc ctg aag ctg aga				2496
Asp Asp Ser Glu Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg				
820		825		830
tat gct gac cag cgc ctg tct tca gac tgt gaa gac cag atc cga atc				2544
Tyr Ala Asp Gln Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile				
835		840		845
att atc cag gag tcc gcc ctg gac tac cgc ctg gat cct cag ctc cag				2592
Ile Ile Gln Glu Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln				
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ctg cac tgc tca gac gag atc tcc agt cta tgt gct gaa gaa gca gca				2640
Leu His Cys Ser Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala				
865		870		880
gcc caa gag cag aca ggt cag gtg gag gag tgc ctc aag gtc aac ctg				2688
Ala Gln Glu Gln Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu				
885		890		895
ctc aag atc aaa aca gaa ttg tgt aaa aag gaa gtg cta aac atg ctg				2736
Leu Lys Ile Lys Thr Glu Leu Cys Lys Glu Val Leu Asn Met Leu				
900		905		910
aag gaa agc aaa gca gac atc ttt gtt gac ccg gta ctt cat act gct				2784
Lys Glu Ser Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala				
915		920		925
tgt gcc ctg gac att aaa cac cac tgc gca gcc atc acc cct ggc cgc				2832
Cys Ala Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg				
930		935		940
ggg cgt caa atg tcc tgt ctc atg gaa gca ctg gag gat aag cgg gtg				2880
Gly Arg Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val				
945		950		955
agg tta cag ccc gag tgc aaa aag cgc ctc aat gac cgg att gag atg				2928
Arg Leu Gln Pro Glu Cys Lys Arg Leu Asn Asp Arg Ile Glu Met				
965		970		975
tgg agt tac gca gca aag gtg gcc cca gca gat ggc ttc tct gat ctt				2976
Trp Ser Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu				
980		985		990
gcc atg caa gta atg acg tct cca tct aag aac tac att ctc tct gtg				3024
Ala Met Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val				
995		1000		1005
atc agt ggg agc atc tgt ata ttg ttc ctg att ggc ctg atg tgt gga				3072
Ile Ser Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly				
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 Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp
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 His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys
 65 70 75 80
 Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met
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 Asp Asp Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg
 100 105 110
 Leu Gly Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu
 115 120 125
 Glu Lys Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln
 130 135 140
 Val Ser Glu Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser
 145 150 155 160
 Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp
 165 170 175
 Asp Arg Glu Arg Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val
 180 185 190
 Tyr Lys Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys
 195 200 205
 Cys Arg Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr
 210 215 220
 Lys Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys
 225 230 235 240
 Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu
 245 250 255
 Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln
 260 265 270
 Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu
 275 280 285
 Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly
 290 295 300
 Glu Ile Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu
 305 310 315 320
 His Cys Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met
 325 330 335
 Asn Cys Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly
 340 345 350

Ala Asp Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val
 355 360 365
 Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu
 370 375 380
 Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys
 385 390 395 400
 Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys
 405 410 415
 Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu
 420 425 430
 Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly
 435 440 445
 Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln
 450 455 460
 Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu
 465 470 475 480
 His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys
 485 490 495
 Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly
 500 505 510
 Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu
 515 520 525
 Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile
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 Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn
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 Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met
 565 570 575
 Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys
 580 585 590
 Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg
 595 600 605
 Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu
 610 615 620
 Cys Pro Asn Ile Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr
 625 630 635 640
 Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser
 645 650 655
 Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu
 660 665 670
 Asp Ile Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile
 675 680 685
 Lys Asn Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu
 690 695 700
 Cys Leu Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys
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 Val Phe Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr
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 Thr Leu Met Arg Val Cys Lys Gln Met Ile Lys Lys Phe Cys Pro Glu
 740 745 750
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 755 760 765
 Glu Leu Met Asp Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile
 770 775 780
 Thr Gln Asn Thr Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys
 785 790 795 800
 Lys Ala Asp Ile Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys

805	810	815	
Asp Asp Ser Glu Leu Glu Gly Gln Val	Ile Ser Cys Leu Lys Leu Arg		
820	825	830	
Tyr Ala Asp Gln Arg Leu Ser Ser Asp Cys Glu Asp Gln	Ile Arg Ile		
835	840	845	
Ile Ile Gln Glu Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln			
850	855	860	
Leu His Cys Ser Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala			
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Ala Gln Glu Gln Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu			
885	890	895	
Leu Lys Ile Lys Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu			
900	905	910	
Lys Glu Ser Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala			
915	920	925	
Cys Ala Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg			
930	935	940	
Gly Arg Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val			
945	950	955	960
Arg Leu Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met			
965	970	975	
Trp Ser Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu			
980	985	990	
Ala Met Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val			
995	1000	1005	
Ile Ser Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly			
1010	1015	1020	
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1025	1030	1035	

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35	40	45	
Phe Val Gly Gln Ala Gly Gly Gly Pro Ala Gly Gln Gln Leu Pro			
50	55	60	
Gln Leu Pro Gln Ser Ser Gln Leu Gln Gln Gln Gln Gln Gln Gln			
65	70	75	80
Gln Gln Gln Pro Gln Pro Pro Gln Pro Pro Phe Pro Ala Gly Gly			
85	90	95	
Pro Pro Arg Arg Gly Gly Ala Gly Gly Gly Trp Lys Leu Ala			
100	105	110	
Glu Glu Glu Ser Cys Arg Glu Asp Val Thr Arg Val Cys Pro Lys His			
115	120	125	
Thr Trp Ser Asn Asn Leu Ala Val Leu Glu Cys Leu Gln Asp Val Arg			
130	135	140	
Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu Leu Trp Asn			
145	150	155	160

Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser Val Ala Arg
 165 170 175
 Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Lys Glu Cys Ala Asp Glu
 180 185 190
 Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp His Arg Gly
 195 200 205
 Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys Met Thr Ala
 210 215 220
 Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met Asp Asp Cys
 225 230 235 240
 Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg Leu Gly Glu
 245 250 255
 Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu Glu Lys Gly
 260 265 270
 Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser Glu
 275 280 285
 Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser Ser Asp Asp
 290 295 300
 Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp Asp Arg Glu
 305 310 315 320
 Arg Phe Cys Glu Asn Thr Gln Ala Cys Glu Gly Arg Val Tyr Lys Cys
 325 330 335
 Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys Cys Arg Glu
 340 345 350
 Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr Lys Val Ser
 355 360 365
 Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys Tyr Arg Cys
 370 375 380
 Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu Ser Tyr Leu
 385 390 395 400
 Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln Val Ser Ser
 405 410 415
 Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu Met Glu Asp
 420 425 430
 Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly Glu Ile Glu
 435 440 445
 His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu His Cys Leu
 450 455 460
 Met Lys Val Val Arg Gly Glu Lys Cys Asn Leu Gly Met Asn Cys Gln
 465 470 475 480
 Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly Ala Asp Tyr
 485 490 495
 Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val Ile Gln Thr
 500 505 510
 Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Ser Ser Cys Leu
 515 520 525
 Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys Glu His Arg
 530 535 540
 Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys Leu Asp Pro
 545 550 555 560
 Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu Cys His Thr
 565 570 575
 His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly Ala Val Phe
 580 585 590
 Ser Cys Leu Tyr Arg Glu Ala Tyr Arg Thr Glu Glu Gln Gly Arg Arg
 595 600 605
 Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu His Gln Arg

610	615	620
Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys Cys Leu Ile		
625	630	635
Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly Gln Glu Leu		640
645	650	655
Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu Cys Arg Asp		
660	665	670
Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile Gln Ile Glu		
675	680	685
Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Thr Phe Cys His		
690	695	700
Asp Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met Glu Cys Leu Ile		
705	710	715
Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys Ala Ile Gly Val		720
725	730	735
Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg Phe Ser Tyr Lys		
740	745	750
Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro Asn Ile		
755	760	765
Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val Arg Asn		
770	775	780
Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys Cys Arg		
785	790	795
Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile Arg Leu		800
805	810	815
Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn Phe Cys		
820	825	830
Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys Leu Lys Glu		
835	840	845
Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys Val Phe Lys Leu		
850	855	860
Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr Thr Leu Met Arg		
865	870	875
Val Cys Lys Gln Met Ile Lys Arg Phe Cys Pro Glu Ala Asp Ser Lys		880
885	890	895
Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser Glu Leu Met Asp		
900	905	910
Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile Thr Gln Asn Thr		
915	920	925
Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys Lys Ala Asp Ile		
930	935	940
Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys Asp Asp Ser Glu		
945	950	955
Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg Tyr Ala Asp Gln		960
965	970	975
Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile Gln Glu		
980	985	990
Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His Cys Ser		
995	1000	1005
Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Ala Gln Glu Gln		
1010	1015	1020
Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys Ile Lys		
1025	1030	1035
Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu Ser Lys		1040
1045	1050	1055
Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala Leu Asp		
1060	1065	1070

Ile Lys His His Cys Ala Ala Leu Thr Pro Gly Arg Gly Arg Gln Met
 1075 1080 1085
 Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val Arg Leu Gln Pro
 1090 1095 1100
 Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met Trp Ser Tyr Ala
 1105 1110 1115 1120
 Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu Ala Met Gln Val
 1125 1130 1135
 Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val Ile Ser Gly Ser
 1140 1145 1150
 Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly Arg Ile Thr Lys
 1155 1160 1165
 Arg Val Thr Arg Glu Leu Lys Asp Arg
 1170 1175

<210> 8
 <211> 1179
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Ala Cys Gly Arg Val Arg Arg Met Phe Arg Leu Ser Ala Ala
 1 5 10 15
 Leu His Leu Leu Leu Leu Phe Ala Ala Gly Ala Glu Lys Leu Pro Gly
 20 25 30
 His Gly Val His Ser Gln Gly Gln Gly Pro Gly Ala Asn Phe Val Ser
 35 40 45
 Phe Val Gly Gln Ala Gly Gly Gly Pro Ala Gly Gln Gln Leu Pro
 50 55 60
 Gln Leu Leu Gln Ser Ser Gln Leu Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Gln Gln Gln Leu Gln Pro Pro Gln Pro Pro Phe Pro Ala Gly Gly
 85 90 95
 Pro Pro Ala Arg Arg Gly Gly Ala Gly Gly Trp Lys Leu
 100 105 110
 Ala Glu Glu Glu Ser Cys Arg Glu Asp Val Thr Arg Val Cys Pro Lys
 115 120 125
 His Thr Trp Ser Asn Asn Leu Ala Val Leu Glu Cys Leu Gln Asp Val
 130 135 140
 Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu Leu Trp
 145 150 155 160
 Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser Val Ala
 165 170 175
 Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Lys Glu Cys Ala Asp
 180 185 190
 Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp His Arg
 195 200 205
 Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys Met Thr
 210 215 220
 Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met Asp Asp
 225 230 235 240
 Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg Leu Gly
 245 250 255
 Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu Glu Lys
 260 265 270
 Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser

275	280	285
Glu Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser Ser Asp		
290	295	300
Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp Asp Arg		
305	310	315
Glu Arg Phe Cys Glu Asn Thr Gln Ala Arg Glu Gly Arg Val Tyr Lys		
325	330	335
Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys Cys Arg		
340	345	350
Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr Lys Val		
355	360	365
Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys Tyr Arg		
370	375	380
Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu Ser Tyr		
385	390	395
Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln Val Ser		
405	410	415
Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu Met Glu		
420	425	430
Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly Glu Ile		
435	440	445
Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu His Cys		
450	455	460
Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met Asn Cys		
465	470	475
Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly Ala Asp		
485	490	495
Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val Ile Gln		
500	505	510
Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu Ser Cys		
515	520	525
Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys Glu His		
530	535	540
Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys Leu Asp		
545	550	555
Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu Cys His		
565	570	575
Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly Ala Val		
580	585	590
Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln Gly Arg		
595	600	605
Arg Leu Leu Asp Pro Ala Leu Gln Asp Lys Cys Leu Ile Asp Leu Gly		
610	615	620
Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly Gln Glu Leu Glu Cys Leu		
625	630	635
Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu His Gln Arg Ala		
645	650	655
Met Asp Val Lys Gln Asp His Leu Asp Asp Leu Val Val Glu Cys Arg		
660	665	670
Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile Gln Ile		
675	680	685
Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn Phe Cys		
690	695	700
His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met Glu Cys		
705	710	715
Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys Ala Ile		
725	730	735

Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg Phe Ser
 740 745 750
 Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro
 755 760 765
 Asn Ile Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val
 770 775 780
 Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys
 785 790 795 800
 Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile
 805 810 815
 Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn
 820 825 830
 Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys Leu
 835 840 845
 Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys Val Phe
 850 855 860
 Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr Thr Leu
 865 870 875 880
 Met Arg Val Cys Lys Gln Met Ile Lys Arg Phe Cys Pro Glu Ala Asp
 885 890 895
 Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser Glu Leu
 900 905 910
 Met Asp Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile Thr Gln
 915 920 925
 Asn Thr Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys Lys Ala
 930 935 940
 Asp Ile Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys Asp Asp
 945 950 955 960
 Ser Glu Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg Tyr Ala
 965 970 975
 Asp Gln Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile
 980 985 990
 Gln Glu Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His
 995 1000 1005
 Cys Ser Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Ala Gln
 1010 1015 1020
 Glu Gln Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys
 1025 1030 1035 1040
 Ile Lys Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu
 1045 1050 1055
 Ser Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala
 1060 1065 1070
 Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg Gly Arg
 1075 1080 1085
 Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val Arg Leu
 1090 1095 1100
 Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met Trp Ser
 1105 1110 1115 1120
 Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu Ala Met
 1125 1130 1135
 Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val Ile Ser
 1140 1145 1150
 Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly Arg Ile
 1155 1160 1165
 Thr Lys Arg Val Thr Arg Glu Leu Lys Asp Arg
 1170 1175

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<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
gcttggagaa aggcctggtg aa 22

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
tggcaattgc ggtacaggac ag 22

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
gcagcttcag cagcaacagc a 21

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
cagctcagcc acccggagaa tg 22

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
gcttggagaa aggcctggtg aa 22

<210> 14

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
tggacttgc ggtacaggac ag 22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
gaacaccgtc tcttagagct gc 22

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
gcttcctgca gagtgtcatt gc 22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
ggaggacgtg ttgaagcttt gc 22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
ccagggcaca agcagtatga ag 22

<210> 19
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 19

caacagcaga caggtcaggt gg

22

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20

ccggaagttc tgggtatg ag

22

<210> 21

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<223> Primer

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attnaacct cactaaaggg

20

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

gtaatacgc tcactatagg gc

22

<210> 23

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

ccggaagttc tgggtatg ag

22

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

gtgaaaggac tcatgaccac agtc

24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

catgtgggcc atgaggtcca ccac

24

<210> 26

<211> 312

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(312)

<223>

<400> 26

agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser

1 5 10

15

tat ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg
Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp

20

25

30

gtg gca gtt ata tca tat gat gga agt aat aaa tac tat gca gac tcc
Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser

35

40

45

gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu

50

55

60

tat ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr

65

70

75

240

tgt gcg agg tcg act acg agg tct tat cct cta tac ggt atg gac gtt
Cys Ala Arg Ser Thr Thr Arg Ser Tyr Pro Leu Tyr Gly Met Asp Val

85

90

95

288

tgg ggc caa ggg aac cct gtc acc
Trp Gly Gln Gly Asn Pro Val Thr

100

312

<210> 27
 <211> 399
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(399)
 <223>

<400> 27

gtg acc tcc tat gtg ctg act cag cca ccc tcg gtg tca gtg gcc cca	48
Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro	
1	5
	10
	15

gga cag acg gcc agt att acc tgt ggg gga aat aac att gga agt aaa	96
Gly Gln Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys	
20	25
	30

agt gtg cac tgg tac cat cag aag cca ggc cag gcc cct gtg ctg gtc	144
Ser Val His Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val	
35	40
	45

gtc tat gat gat agc gac cgg ccc tca ggg atc cct gag cga ttc tct	192
Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser	
50	55
	60

ggc tcc aac tct ggg aac acg gcc acc ctg acc atc acc agg gtc gaa	240
Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu	
65	70
	75
	80

gcc ggg gat gag gcc gac tat tac tgt cag gtg tgg gat agt agt agt	288
Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser	
85	90
	95

gat ctc aat tgg gtg ttc ggc gga agg acc caa gct gac cgt cct acg	336
Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala Asp Arg Pro Thr	
100	105
	110

tca gcc caa ggc tgc ccc tcc ggt cac tct gtt ccc cgc ccc cct ctg	384
Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro Pro Leu	
115	120
	125

aag agc ttc aag ctt	399
Lys Ser Phe Lys Leu	
130	

<210> 28
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 28

Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser	
1	5
	10
	15
Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp	

20 25 30
Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser
35 40 45
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
50 55 60
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
65 70 75 80
Cys Ala Arg Ser Thr Thr Arg Ser Tyr Pro Leu Tyr Gly Met Asp Val
85 90 95
Trp Gly Gln Gly Asn Pro Val Thr
100

<210> 29

<211> 133

<212> PRT

<213> Homo sapiens

<400> 29

Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro
1 5 10 15
Gly Gln Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys
20 25 30
Ser Val His Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val
35 40 45
Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser
50 55 60
Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu
65 70 75 80
Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser
85 90 95
Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala Asp Arg Pro Thr
100 105 110
Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro Pro Leu
115 120 125
Lys Ser Phe Lys Leu
130

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30

caagagcaga caggtcaggt gg

22